

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/533,277
Source: PUT
Date Processed by STIC: 3/6/06

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PCT

RAW SEQUENCE LISTING

DATE: 03/06/2006

PATENT APPLICATION: US/10/533,277

TIME: 15:11:32

Input Set : F:\404uspc.app.txt

Output Set: N:\CRF4\03062006\J533277.raw

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3 <110> APPLICANT: Mitsuhashi, Tadayoshi
5 <120> TITLE OF INVENTION: METHODS FOR DETERMINING GENETIC RESISTANCE OF PIGS
6     TO DISEASES CAUSED BY RNA VIRUSES
8 <130> FILE REFERENCE: 690107.404USPC
10 <140> CURRENT APPLICATION NUMBER: US 10/533,277
C--> 11 <141> CURRENT FILING DATE: 2005-04-28
13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/13767
14 <151> PRIOR FILING DATE: 2003-10-28
16 <150> PRIOR APPLICATION NUMBER: JP 2002-313076
17 <151> PRIOR FILING DATE: 2002-10-28
19 <160> NUMBER OF SEQ ID NOS: 11
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2545
25 <212> TYPE: DNA
26 <213> ORGANISM: Sus scrofa
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (101)..(2092)
32 <220> FEATURE:
33 <221> NAME/KEY: polyA_signal
34 <222> LOCATION: (2517)..(2522)
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39 aaaggaaggt acatttcagc tgaactgacg aaggaggaag atg gtt tat tcc agc 115
40                                     Met Val Tyr Ser Ser
41                                     1           5
43 tgt gaa agt aaa gaa cct gat tca gtt tct gca tcc aat cac ctg tta 163
44 Cys Glu Ser Lys Glu Pro Asp Ser Val Ser Ala Ser Asn His Leu Leu
45           10           15           20
47 cta aat ggg aat gat gaa ttg gtg gag aaa agt cac aaa aca ggg cct 211
48 Leu Asn Gly Asn Asp Glu Leu Val Glu Lys Ser His Lys Thr Gly Pro
49           25           30           35
51 gag aac aac ctg tac agc cag tac gag gag aaa gtg cgg ccc tgc atc 259
52 Glu Asn Asn Leu Tyr Ser Gln Tyr Glu Glu Lys Val Arg Pro Cys Ile
53           40           45           50
55 gac ctc atc gac tca ctg cgg gcc ctg ggc gtg gag cag gac ctg gcc 307
56 Asp Leu Ile Asp Ser Leu Arg Ala Leu Gly Val Glu Gln Asp Leu Ala
57           55           60           65
59 ctg ccc gcc atc gcc gtc atc ggg gac cag agt tcg ggc aag agc tcc 355
60 Leu Pro Ala Ile Ala Val Ile Gly Asp Gln Ser Ser Gly Lys Ser Ser
61 70           75           80           85
63 gtg ctg gag gcc ctg tcg ggg gtc gct ctc ccc aga ggc agc gga att 403

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65                               90                               95                               100
67 gtg aca aga tgc cct ctt gtg ctg aaa ttg aaa aaa ctc gtg aac gaa 451
68 Val Thr Arg Cys Pro Leu Val Leu Lys Leu Lys Lys Leu Val Asn Glu
69                               105                               110                               115
71 gaa gac gaa tgg aag ggc aaa gtc agt tac cgg gac agc gag att gag 499
72 Glu Asp Glu Trp Lys Gly Lys Val Ser Tyr Arg Asp Ser Glu Ile Glu
73                               120                               125                               130
75 ctt tca gat gct tcg cag gtg gaa aag gaa gtc agc gca gcc cag att 547
76 Leu Ser Asp Ala Ser Gln Val Glu Lys Glu Val Ser Ala Ala Gln Ile
77                               135                               140                               145
79 gcc atc gct ggg gaa ggc gtg gga atc agt cat gag cta atc agt ctg 595
80 Ala Ile Ala Gly Glu Gly Val Gly Ile Ser His Glu Leu Ile Ser Leu
81 150                               155                               160                               165
83 gag gtc agc tcc cct cat gtc cca gat ctg acc ctc ata gac ctt cct 643
84 Glu Val Ser Ser Pro His Val Pro Asp Leu Thr Leu Ile Asp Leu Pro
85                               170                               175                               180
87 ggc atc acc agg gta gct gta ggc aat cag cca tac gac atc gaa tac 691
88 Gly Ile Thr Arg Val Ala Val Gly Asn Gln Pro Tyr Asp Ile Glu Tyr
89                               185                               190                               195
91 cag atc aag tct ctg atc aag aag tac atc tgt aag cag gag acc atc 739
92 Gln Ile Lys Ser Leu Ile Lys Lys Tyr Ile Cys Lys Gln Glu Thr Ile
93                               200                               205                               210
95 aac ttg gtg gtg gtc ccc tgt aac gtg gac att gcc acc acg gag gcg 787
96 Asn Leu Val Val Val Pro Cys Asn Val Asp Ile Ala Thr Thr Glu Ala
97                               215                               220                               225
99 ctg cgc atg gcc cag gag gtg gac ccc gaa gga gac agg acc atc ggg 835
100 Leu Arg Met Ala Gln Glu Val Asp Pro Glu Gly Asp Arg Thr Ile Gly
101 230                               235                               240                               245
103 atc ttg acg aag ccg gat ctg gtg gac aaa ggc act gag gac aag ata 883
104 Ile Leu Thr Lys Pro Asp Leu Val Asp Lys Gly Thr Glu Asp Lys Ile
105                               250                               255                               260
107 gtg gac gtg gcg aga aac ctg gtc ttc cac ctg aag aag ggc tac atg 931
108 Val Asp Val Ala Arg Asn Leu Val Phe His Leu Lys Lys Gly Tyr Met
109                               265                               270                               275
111 att gtc aag tgc agg ggc cag cag gac atc cag gag cag ctg agc ctg 979
112 Ile Val Lys Cys Arg Gly Gln Gln Asp Ile Gln Glu Gln Leu Ser Leu
113                               280                               285                               290
115 gcc aag gcc ctg cag aag gag cag gcc ttc ttt gaa aac cac gca cat 1027
116 Ala Lys Ala Leu Gln Lys Glu Gln Ala Phe Phe Glu Asn His Ala His
117                               295                               300                               305
119 ttc agg gat ctt ctg gag gaa ggg cgg gcc acg atc ccc tgc ctg gca 1075
120 Phe Arg Asp Leu Leu Glu Glu Gly Arg Ala Thr Ile Pro Cys Leu Ala
121 310                               315                               320                               325
123 gaa aga ctg acc tct gaa ctc atc atg cac atc tgt aaa act ctg ccc 1123
124 Glu Arg Leu Thr Ser Glu Leu Ile Met His Ile Cys Lys Thr Leu Pro
125                               330                               335                               340
127 ctg tta gaa aac caa ata aaa gag agt cac cag aaa ata aca gag gag 1171
128 Leu Leu Glu Asn Gln Ile Lys Glu Ser His Gln Lys Ile Thr Glu Glu

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129		345		350		355											
131	tta	cag	aag	tat	ggc	tcc	gat	att	cca	gag	gat	gaa	agc	ggg	aag	atg	1219
132	Leu	Gln	Lys	Tyr	Gly	Ser	Asp	Ile	Pro	Glu	Asp	Glu	Ser	Gly	Lys	Met	
133			360					365						370			
135	ttt	ttt	ctg	ata	gat	aaa	atc	gat	gca	ttt	aat	agt	gat	atc	act	gct	1267
136	Phe	Phe	Leu	Ile	Asp	Lys	Ile	Asp	Ala	Phe	Asn	Ser	Asp	Ile	Thr	Ala	
137		375					380					385					
139	ttg	ata	caa	gga	gag	gaa	ctg	gtg	gtg	gag	tac	gag	tgt	cgg	ctg	ttt	1315
140	Leu	Ile	Gln	Gly	Glu	Glu	Leu	Val	Val	Glu	Tyr	Glu	Cys	Arg	Leu	Phe	
141	390					395					400				405		
143	acc	aag	atg	cga	aat	gag	ttc	tgc	aga	tgg	agt	gct	gtg	gtt	gaa	aag	1363
144	Thr	Lys	Met	Arg	Asn	Glu	Phe	Cys	Arg	Trp	Ser	Ala	Val	Val	Glu	Lys	
145				410					415					420			
147	aat	ttc	aaa	aat	ggt	tat	gac	gcc	ata	tgt	aaa	caa	atc	cag	ctc	ttc	1411
148	Asn	Phe	Lys	Asn	Gly	Tyr	Asp	Ala	Ile	Cys	Lys	Gln	Ile	Gln	Leu	Phe	
149			425						430					435			
151	gaa	aat	cag	tac	agg	ggg	aga	gag	ttg	cca	ggg	ttt	gtg	aat	tat	aag	1459
152	Glu	Asn	Gln	Tyr	Arg	Gly	Arg	Glu	Leu	Pro	Gly	Phe	Val	Asn	Tyr	Lys	
153		440					445					450					
155	aca	ttt	gaa	acc	atc	att	aag	aag	cag	gtc	agt	gtc	ctg	gaa	gag	cca	1507
156	Thr	Phe	Glu	Thr	Ile	Ile	Lys	Lys	Gln	Val	Ser	Val	Leu	Glu	Glu	Pro	
157		455				460					465						
159	gcc	gtg	gac	atg	ctg	cac	aca	gtg	act	gat	tta	gtc	cgg	ctc	gcc	ttc	1555
160	Ala	Val	Asp	Met	Leu	His	Thr	Val	Thr	Asp	Leu	Val	Arg	Leu	Ala	Phe	
161	470				475					480					485		
163	aca	gat	gtt	tca	gaa	aca	aat	ttt	aat	gaa	ttt	ttc	aac	ctc	cac	aga	1603
164	Thr	Asp	Val	Ser	Glu	Thr	Asn	Phe	Asn	Glu	Phe	Phe	Asn	Leu	His	Arg	
165			490						495					500			
167	act	gcc	aag	tcc	aaa	att	gaa	gac	att	aaa	tta	gaa	caa	gaa	aaa	gaa	1651
168	Thr	Ala	Lys	Ser	Lys	Ile	Glu	Asp	Ile	Lys	Leu	Glu	Gln	Glu	Lys	Glu	
169			505						510					515			
171	gct	gag	acg	tcg	atc	cgg	ctc	cac	ttc	caa	atg	gag	cag	atc	gtg	tac	1699
172	Ala	Glu	Thr	Ser	Ile	Arg	Leu	His	Phe	Gln	Met	Glu	Gln	Ile	Val	Tyr	
173		520					525					530					
175	tgc	cag	gac	cag	gtc	tat	cgg	ggc	gcg	ctg	cag	aag	gtc	aga	gag	aag	1747
176	Cys	Gln	Asp	Gln	Val	Tyr	Arg	Gly	Ala	Leu	Gln	Lys	Val	Arg	Glu	Lys	
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180	Glu	Ala	Glu	Glu	Glu	Lys	Asn	Arg	Lys	Ser	Asn	Gln	Tyr	Phe	Leu	Ser	
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183	tcg	ccg	gcc	ccc	tcc	tca	gac	ccc	tcc	ata	gcc	gag	atc	ttt	cag	cac	1843
184	Ser	Pro	Ala	Pro	Ser	Ser	Asp	Pro	Ser	Ile	Ala	Glu	Ile	Phe	Gln	His	
185			570						575					580			
187	ctg	att	gcc	tac	cat	cag	gag	gtc	ggc	aag	cgc	atc	tcc	agc	cac	atc	1891
188	Leu	Ile	Ala	Tyr	His	Gln	Glu	Val	Gly	Lys	Arg	Ile	Ser	Ser	His	Ile	
189			585						590					595			
191	cct	ctg	atc	atc	cag	ttc	ttc	atc	ctc	cgg	acc	ttt	ggg	cag	cag	ctg	1939
192	Pro	Leu	Ile	Ile	Gln	Phe	Phe	Ile	Leu	Arg	Thr	Phe	Gly	Gln	Gln	Leu	
193			600					605						610			

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195 cag aag agc atg ctg cag ctg ctg cag aac aag gac caa tac gac tgg 1987
196 Gln Lys Ser Met Leu Gln Leu Leu Gln Asn Lys Asp Gln Tyr Asp Trp
197      615                      620                      625
199 ctc ctg agg gag cgc agt gac acc agc gac aag agg aag ttc ctg aag 2035
200 Leu Leu Arg Glu Arg Ser Asp Thr Ser Asp Lys Arg Lys Phe Leu Lys
201 630                      635                      640                      645
203 gag cgg ctg atg cgg ctg acc cag gct cgg cgc cgg ctc gcc aag ttc 2083
204 Glu Arg Leu Met Arg Leu Thr Gln Ala Arg Arg Arg Leu Ala Lys Phe
205                      650                      655                      660
207 cca ggc tga accggactct ccaggcggcc cggggtctcc agggcacgtc 2132
208 Pro Gly
210 tccaggcaac gaggaccaac ctccttcctt aacagactag catcatgagc tcctgtttcg 2192
212 cacatcctcc tgtggttagt agactctaaa gccaccgtcc ctgctgttag tggctgagga 2252
214 cttagcaaga agctgtgata agcacgctgg ctgcaagcat caggccattt acttgaatga 2312
216 gccccgcaaa cgcttcgcct cccgcgcctc tctccatccc tctctccatc cttctctcca 2372
218 tccctgtata ggatactggg cccgcgatag catcatagaa gggtcattct ggtttctgta 2432
220 caagcctttc acgccaatg tcttaggggc attacagcca cctgtgtgga tggatgcaca 2492
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227 <212> TYPE: PRT
228 <213> ORGANISM: Sus scrofa
230 <400> SEQUENCE: 2
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235 20 25 30
237 His Lys Thr Gly Pro Glu Asn Asn Leu Tyr Ser Gln Tyr Glu Glu Lys
238 35 40 45
240 Val Arg Pro Cys Ile Asp Leu Ile Asp Ser Leu Arg Ala Leu Gly Val
241 50 55 60
243 Glu Gln Asp Leu Ala Leu Pro Ala Ile Ala Val Ile Gly Asp Gln Ser
244 65 70 75 80
246 Ser Gly Lys Ser Ser Val Leu Glu Ala Leu Ser Gly Val Ala Leu Pro
247 85 90 95
249 Arg Gly Ser Gly Ile Val Thr Arg Cys Pro Leu Val Leu Lys Leu Lys
250 100 105 110
252 Lys Leu Val Asn Glu Glu Asp Glu Trp Lys Gly Lys Val Ser Tyr Arg
253 115 120 125
255 Asp Ser Glu Ile Glu Leu Ser Asp Ala Ser Gln Val Glu Lys Glu Val
256 130 135 140
258 Ser Ala Ala Gln Ile Ala Ile Ala Gly Glu Gly Val Gly Ile Ser His
259 145 150 155 160
261 Glu Leu Ile Ser Leu Glu Val Ser Ser Pro His Val Pro Asp Leu Thr
262 165 170 175
264 Leu Ile Asp Leu Pro Gly Ile Thr Arg Val Ala Val Gly Asn Gln Pro
265 180 185 190
267 Tyr Asp Ile Glu Tyr Gln Ile Lys Ser Leu Ile Lys Lys Tyr Ile Cys
268 195 200 205

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270 Lys Gln Glu Thr Ile Asn Leu Val Val Val Pro Cys Asn Val Asp Ile
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273 Ala Thr Thr Glu Ala Leu Arg Met Ala Gln Glu Val Asp Pro Glu Gly
274 225      230      235      240
276 Asp Arg Thr Ile Gly Ile Leu Thr Lys Pro Asp Leu Val Asp Lys Gly
277      245      250      255
279 Thr Glu Asp Lys Ile Val Asp Val Ala Arg Asn Leu Val Phe His Leu
280      260      265      270
282 Lys Lys Gly Tyr Met Ile Val Lys Cys Arg Gly Gln Gln Asp Ile Gln
283      275      280      285
285 Glu Gln Leu Ser Leu Ala Lys Ala Leu Gln Lys Glu Gln Ala Phe Phe
286      290      295      300
288 Glu Asn His Ala His Phe Arg Asp Leu Leu Glu Glu Gly Arg Ala Thr
289 305      310      315      320
291 Ile Pro Cys Leu Ala Glu Arg Leu Thr Ser Glu Leu Ile Met His Ile
292      325      330      335
294 Cys Lys Thr Leu Pro Leu Leu Glu Asn Gln Ile Lys Glu Ser His Gln
295      340      345      350
297 Lys Ile Thr Glu Glu Leu Gln Lys Tyr Gly Ser Asp Ile Pro Glu Asp
298      355      360      365
300 Glu Ser Gly Lys Met Phe Phe Leu Ile Asp Lys Ile Asp Ala Phe Asn
301      370      375      380
303 Ser Asp Ile Thr Ala Leu Ile Gln Gly Glu Glu Leu Val Val Glu Tyr
304 385      390      395      400
306 Glu Cys Arg Leu Phe Thr Lys Met Arg Asn Glu Phe Cys Arg Trp Ser
307      405      410      415
309 Ala Val Val Glu Lys Asn Phe Lys Asn Gly Tyr Asp Ala Ile Cys Lys
310      420      425      430
312 Gln Ile Gln Leu Phe Glu Asn Gln Tyr Arg Gly Arg Glu Leu Pro Gly
313      435      440      445
315 Phe Val Asn Tyr Lys Thr Phe Glu Thr Ile Ile Lys Lys Gln Val Ser
316      450      455      460
318 Val Leu Glu Glu Pro Ala Val Asp Met Leu His Thr Val Thr Asp Leu
319 465      470      475      480
321 Val Arg Leu Ala Phe Thr Asp Val Ser Glu Thr Asn Phe Asn Glu Phe
322      485      490      495
324 Phe Asn Leu His Arg Thr Ala Lys Ser Lys Ile Glu Asp Ile Lys Leu
325      500      505      510
327 Glu Gln Glu Lys Glu Ala Glu Thr Ser Ile Arg Leu His Phe Gln Met
328      515      520      525
330 Glu Gln Ile Val Tyr Cys Gln Asp Gln Val Tyr Arg Gly Ala Leu Gln
331      530      535      540
333 Lys Val Arg Glu Lys Glu Ala Glu Glu Glu Lys Asn Arg Lys Ser Asn
334 545      550      555      560
336 Gln Tyr Phe Leu Ser Ser Pro Ala Pro Ser Ser Asp Pro Ser Ile Ala
337      565      570      575
339 Glu Ile Phe Gln His Leu Ile Ala Tyr His Gln Glu Val Gly Lys Arg
340      580      585      590
342 Ile Ser Ser His Ile Pro Leu Ile Ile Gln Phe Phe Ile Leu Arg Thr

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date